

	Pro	Leu	Phe	Gly	Ala	Gly	Ser	Ile	Ser	Ser	Gly	Glu	Leu	Tyr	Ile	Asp	
	595							600					605				
5	Lys	Ile	Glu	Ile	Ile	Leu	Ala	Asp	Ala	Thr	Phe	Glu	Ala	Glu	Ser	Asp	
	610						615					620					
	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	Asn	Ala	Leu	Phe	Thr	Ser	Ser	Asn	
	625					630					635					640	
10	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	
					645					650					655		
	Ser	Asn	Leu	Val	Asp	Cys	Leu	Ser	Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	
15				660					665					670			
	Arg	Glu	Leu	Ser	Glu	Lys	Val	Lys	His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	
		675						680					685				
20	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	Phe	Arg	Gly	Ile	Asn	Arg	Gln	Pro	
	690						695					700					
	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	
	705					710					715					720	
25	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu	Pro	Gly	Thr	Val	Asp	Glu	
					725					730					735		
	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	
				740					745					750			
	Ala	Tyr	Thr	Arg	Tyr	Glu	Leu	Arg	Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	
		755						760					765				
35	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	Asn	Ala	Lys	His	Glu	Ile	Val	Asn	
	770						775					780					
	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	Pro	Leu	Ser	Ala	Gln	Ser	Pro	Ile	
	785					790					795					800	
40	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	
				805						810					815		
	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	His	
45				820					825					830			
	Ser	His	His	Phe	Thr	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	
		835						840					845				
50	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	
	850						855					860					
	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	Lys	Pro	Leu	Leu	
	865					870					875					880	

	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	
					885					890					895		
5	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	
					900				905					910			
	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	
					915				920					925			
10	Gln	Val	Asp	Thr	Asn	Ile	Ala	Met	Ile	His	Ala	Ala	Asp	Lys	Arg	Val	
					930				935				940				
	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	
15					945				950				955			960	
	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	
					965					970					975		
20	Tyr	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	
					980					985				990			
	Asn	Gly	Leu	Leu	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Glu	Glu	
					995				1000					1005			
25	Gln	Asn	Asn	His	Arg	Ser	Val	Leu	Val	Ile	Pro	Glu	Trp	Glu	Ala	Glu	
					1010				1015				1020				
	Val	Ser	Gln	Glu	Val	Arg	Val	Cys	Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	
					1025				1030				1035			1040	
30	Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His	
					1045					1050					1055		
	Glu	Ile	Glu	Asp	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu	
					1060					1065					1070		
	Glu	Glu	Val	Tyr	Pro	Asn	Asn	Thr	Val	Thr	Cys	Asn	Asn	Tyr	Thr	Gly	
					1075					1080				1085			
40	Thr	Gln	Glu	Glu	Tyr	Glu	Gly	Thr	Tyr	Thr	Ser	Arg	Asn	Gln	Gly	Tyr	
					1090					1095				1100			
	Asp	Glu	Ala	Tyr	Gly	Asn	Asn	Pro	Ser	Val	Pro	Ala	Asp	Tyr	Ala	Ser	
45					1105					1110				1115		1120	
	Val	Tyr	Glu	Glu	Lys	Ser	Tyr	Thr	Asp	Gly	Arg	Arg	Glu	Asn	Pro	Cys	
					1125						1130				1135		
50	Glu	Ser	Asn	Arg	Gly	Tyr	Gly	Asp	Tyr	Thr	Pro	Leu	Pro	Ala	Gly	Tyr	
					1140					1145					1150		
	Val	Thr	Lys	Asp	Leu	Glu	Tyr	Phe	Pro	Glu	Thr	Asp	Lys	Val	Trp	Ile	
					1155					1160					1165		

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

5 Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
1 5 10 15	
AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
20 25 30	
TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
35 40 45	
TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
50 55 60	
GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
65 70 75 80	
CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
85 90 95	
GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
100 105 110	
TTT AAA GAA TGG GAA GAT GAT CCT CAT AAT CCC ACA ACC AGG ACC AGA	384
Phe Lys Glu Trp Glu Asp Asp Pro His Asn Pro Thr Thr Arg Thr Arg	
115 120 125	